

## SEQUENCE LISTING

&lt;110&gt; Kunsch et al

&lt;120&gt; Human Hepatoma-Derived Growth Factor-2

&lt;130&gt; PF198D1C1

&lt;140&gt; Unassigned

&lt;141&gt; 2001-11-15

&lt;150&gt; 09/263,625

&lt;151&gt; 1999-03-05

&lt;150&gt; 08/464,600

&lt;151&gt; 1995-06-05

&lt;160&gt; 7

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 3202

&lt;212&gt; DNA

&lt;213&gt; human

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (34) .. (780)

&lt;223&gt;

&lt;400&gt; 1

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ctc ggc gac ttg gtg tgg ggg aaa ctc ggc cga tat cct cct tgg cca      102
Leu Gly Asp Leu Val Trp Gly Lys Leu Gly Arg Tyr Pro Pro Trp Pro
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gga aag att gtt aat cca cca aag gac ttg aag aaa cct cgc gga aag      150
Gly Lys Ile Val Asn Pro Pro Lys Asp Leu Lys Lys Pro Arg Gly Lys
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```

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aaa tgc ttc ttt gtg aaa ttt ttt gga aca gaa gat cat gcc tgg atc      198
Lys Cys Phe Phe Val Lys Phe Phe Gly Thr Glu Asp His Ala Trp Ile
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aaa gtg gaa cag ctg aag cca tat cat gct cat aaa gag gaa atg ata      246
Lys Val Glu Gln Leu Lys Pro Tyr His Ala His Lys Glu Glu Met Ile
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aaa att aac aag ggt aaa cga ttc cag caa gcg gta gat gct gtc gaa      294
Lys Ile Asn Lys Gly Lys Arg Phe Gln Gln Ala Val Asp Ala Val Glu
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gag ttc ctc agg aga gcc aaa ggg aaa gac cag acg tca tcc cac aat      342
Glu Phe Leu Arg Arg Ala Lys Gly Lys Asp Gln Thr Ser Ser His Asn
      90                      95                      100

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0098755-11504

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120			125						130			135						
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Leu Lys Lys Pro Arg Gly Lys Lys Cys Phe Phe Val Lys Phe Phe Gly  
 35 40 45

Thr Glu Asp His Ala Trp Ile Lys Val Glu Gln Leu Lys Pro Tyr His  
 50 55 60

Ala His Lys Glu Glu Met Ile Lys Ile Asn Lys Gly Lys Arg Phe Gln  
 65 70 75 80

Gln Ala Val Asp Ala Val Glu Glu Phe Leu Arg Arg Ala Lys Gly Lys  
 85 90 95

Asp Gln Thr Ser Ser His Asn Ser Ser Asp Asp Lys Asn Arg Arg Asn  
 100 105 110

Ser Ser Glu Glu Arg Ser Arg Pro Asn Ser Gly Asp Glu Lys Arg Lys  
 115 120 125

Leu Ser Leu Ser Glu Gly Lys Val Lys Lys Asn Met Gly Glu Gly Lys  
 130 135 140

Lys Arg Val Ser Ser Gly Ser Ser Glu Arg Gly Ser Lys Ser Pro Leu  
 145 150 155 160

Lys Arg Ala Gln Glu Gln Ser Pro Arg Lys Arg Gly Arg Pro Pro Lys  
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Asp Glu Lys Asp Leu Thr Ile Pro Glu Ser Ser Thr Val Lys Gly Met  
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Met Ala Gly Pro Met Ala Ala Phe Lys Trp Gln Pro Thr Ala Ser Glu  
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Pro Val Lys Asp Ala Asp Pro His Phe His His Phe Leu Leu Ser Gln  
 210 215 220

0000755-11101

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[illegible]

